

09/701618

529 Rec'd PCT/PTC 01 DEC 2000

SEQUENCE PROTOCOL

(1) GENERAL INDICATIONS:

(i) APPLICANT:

- (A) NAME: Deutsches Krebsforschungszentrum
- (B) STREET: Im Neuenheimer Feld 280
- (C) TOWN: Heidelberg
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 69120

(ii) TITLE OF THE INVENTION: Method for Triggering Apoptosis in Cells

(iii) NUMBER OF SEQUENCES: 10

(iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, version #1.30  
(EPO)

(v) DATA OF THE CURRENT APPLICATION: not yet known

(vi) DATA OF THE PRIOR APPLICATION:

APPLICATION NUMBER: DE 198 24 811.3  
FILING DATE: June 3, 1998

(2) INDICATIONS AS TO ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 base pairs
- (B) KIND: nucleotide
- (C) STRAND FORM: single strand
- (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(ix) CHARACTERISTIC:

- (A) NAME/KEY: CDS
- (B) POSITION: 118..540

(ix) CHARACTERISTIC:

- (A) NAME/KEY: mat\_peptide
- (B) Position: 118..540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTTTCCGGGA GACTGGAGTC GAAGGCCGTG AGTATTTTCT AAGCCAGTGT TTAGAGAGTA	60
TGTGAGGCAA GAGTACCTAT AGAACCCGGA GGAGGGTGAG GAGCAGAGCT GGCCATA	117
ATG GCA GGT GAA GAA ATT AAT GAA GAC TAT CCA GTA GAA ATT CAC GAG Met Ala Gly Glu Glu Ile Asn Glu Asp Tyr Pro Val Glu Ile His Glu	165
1 5 10 15	
TAT TTG TCA GCG TTT GAG AAT TCC ATT GGT GCT GTG GAT GAG ATG CTG Tyr Leu Ser Phe Glu Asn Ser Ile Gly Ala Val Asp Glu Met Leu	213
20 25 30	
AAG ACC ATG ATG TCT GTT TCT AGA AAT GAG TTG TTG CAG AAG TTG GAT Lys Thr Met Met Ser Val Ser Arg Asn Glu Leu Leu Gln Lys Leu Asp	261
35 40 45	
CCA CTT GAA CAA GCA AAA GTG GAT TTG GTT TCT GCA TAC ACA TTA AAT Pro Leu Glu Gln Ala Lys Val Asp Leu Val Ser Ala Tyr Thr Leu Asn	309
50 55 60	
TCA ATG TTT TGG GTT TAT TTG GCA ACC CAA GGA GTT AAT CCT AAG GAA Ser Met Phe Trp Val Tyr Leu Ala Thr Gln Gly Val Asn Pro Lys Glu	357
65 70 75 80	
CAT CCA GTA AAA CAG GAA TTG GAA AGA ATC AGA GTA TAT ATG AAC AGA His Pro Val Lys Gln Glu Leu Glu Arg Ile Arg Val Tyr Met Asn Arg	405
85 90 95	
GTC AAG GAA ATA ACA GAC AAG AAA AAG GCT GGC AAG CTG GAC AGA GGT Val Lys Glu Ile Thr Asp Lys Lys Lys Ala Gly Lys Leu Asp Arg Gly	453
100 105 110	
GCA GCT TCA AGA TTT GTA AAA AAT GCC CTC TGG GAA CCA AAA TCG AAA Ala Ala Ser Arg Phe Val Lys Asn Ala Leu Trp Glu Pro Lys Ser Lys	501
115 120 125	
AAT GCA TCA AAA GTT GCC AAT AAA GGA AAA AGT AAA AGT TAACTTTTTG Asn Ala Ser Lys Val Ala Asn Lys Gly Lys Ser Lys Ser	550
130 135 140	
GTTTTGATGT ACACATATTC AAAAAGTACA TTAATATGTA ATCACAGTAA TATGTAAAGC	610
TAAATACTTC CTCTCCAAAG ATCATTATCT TTATTGATTA GCACTGAGGA TTTTAACATT	670
GTGATATATT ATATATTTAT AATTTACCAT CTCTTGATGA GACTCTTATT TCTTTATATA	730
GGTCAGTCTT GCAAGTACCA TTTTATAAGC AGCTGTGAAA TTTAAGTGAA ATGTTCTTTG	790
TAAACATTTG TACTATTTTA AATGAATAAT GACCTTATGA AGTATGCTAT CTGTAGGCTG	850
AAATTATAGG TACATCTGTT TTCACTATAT GATATTAAGA AAGCGTGAAT GACTTAAATG	910
TTCATTTTTT TCTGTATAGA TACTTTATCA TGTTTTCATG ATTTTAGGAA TTAGTGCTTT	970

GTTGATATTC AAAGTGTGAA ACTAAAAGTT TATGGTTGTA CTTTAATTCT TGGCATGTTG 1030  
 CCTCTATGTC CCATTTAAAA TAAAATACAT TCTCATTAAC TTTAGATGGG AAATAAGGTT 1090  
 GTATGTTGAT GGATGAATTT TGGCATGATG ACTGTACTCT CAATAAAGGC TGAAAAATGTT 1150  
 GTAAAA 1156

(2) INDICATIONS AS TO ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) KIND: amino acid
- (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

Met	Ala	Gly	Glu	Glu	Ile	Asn	Glu	Asp	Tyr	Pro	Val	Glu	Ile	His	Glu	1	5	10	15
Tyr	Leu	Ser	Ala	Phe	Glu	Asn	Ser	Ile	Gly	Ala	Val	Asp	Glu	Met	Leu	20	25	30	
Lys	Thr	Met	Met	Ser	Val	Ser	Arg	Asn	Glu	Leu	Leu	Gln	Lys	Leu	Asp	35	40	45	
Pro	Leu	Glu	Gln	Ala	Lys	Val	Asp	Leu	Val	Ser	Ala	Tyr	Thr	Leu	Asn	50	55	60	
Ser	Met	Phe	Trp	Val	Tyr	Leu	Ala	Thr	Gln	Gly	Val	Asn	Pro	Lys	Glu	65	70	75	80
His	Pro	Val	Lys	Gln	Glu	Leu	Glu	Arg	Ile	Arg	Val	Tyr	Met	Asn	Arg	85	90	95	
Val	Lys	Glu	Ile	Thr	Asp	Lys	Lys	Lys	Ala	Gly	Lys	Leu	Asp	Arg	Gly	100	105	110	
Ala	Ala	Ser	Arg	Phe	Val	Lys	Asn	Ala	Leu	Trp	Glu	Pro	Lys	Ser	Lys	115	120	125	
Asn	Ala	Ser	Lys	Val	Ala	Asn	Lys	Gly	Lys	Ser	Lys	Ser				130	135	140	

(2) INDICATIONS AS TO ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1040 base pairs  
 (B) KIND: nucleotide  
 (C) STRAND FORM: single strand  
 (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: cDNA

(iii) HYPHETICAL: no

(iv) ANTISENSE: no

- (ix) CHARACTERISTIC:  
 (A) NAME/KEY: CDS  
 (B) POSITION: 78..500

- (ix) CHARACTERISTIC:  
 (A) NAME/KEY: mat\_peptide  
 (B) Position: 78..500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGAAGCCGT GTCATGGCGT CATCATCGTG CGACCTATTT CCCGGAGACA GCGCTCCACG	60
GTATTGAGTT GGTCACA ATG GCA GGT GAA GAA ATG AAT GAA GAT TAT CCC	110
Met Ala Gly Glu Met Asn Glu Asp Tyr Pro	
1 5 10	
GTA GAA ATT CAC GAG TCT TTA ACA GCC CTG GAG AGC TCC CTG GGT GCT	158
Val Glu Ile His Glu Ser Leu Thr Ala Leu Glu Ser Ser Leu Gly Ala	
15 20 25	
GTG GAC GAC ATG CTG AAG ACC ATG ATG GCT GTT TCT AGA AAC GAG TTG	206
Val Asp Asp Met Leu Lys Thr Met Met Ala Val Ser Arg Asn Glu Leu	
30 35 40	
TTG CAG AAG TTG GAC CCA TTG GAA CAA GCA AAG GTG GAT TTA GTT TCT	254
Leu Gln Lys Leu Asp Pro Leu Glu Gln Ala Lys Val Asp Leu Val Ser	
45 50 55	
GCA TAC ACC TTA AAT TCA ATG TTT TGG GTT TAT TTG GCA ACT CAA GGA	302
Ala Tyr Thr Leu Asn Ser Met Phe Trp Val Tyr Leu Ala Thr Gln Gly	
60 65 70 75	
GTT AAT CCC AAA GAG CAT CCA GTG AAG CAG GAA CTG GAA AGA ATC AGA	350
Val Asn Pro Lys Glu His Pro Val Lys Gln Glu Leu Glu Arg Ile Arg	
80 85 90	
GTC TAC ATG AAC AGA GTT AAA GAA ATA ACA GAC AAG AAG AAG GCT GCC	398
Val Tyr Met Asn Arg Val Lys Glu Ile Thr Asp Lys Lys Lys Ala Ala	
95 100 105	
AAG CTG GAC AGA GGT GCT GCT TCG AGA TTT GTC AAG AAG GCA CTC TGG	446

Lys Leu Asp Arg Gly Ala Ala Ser Arg Phe Val Lys Lys Ala Leu Trp  
 110 115 120

GAA CCC AAA CGA AAA AGC ACA CCA AAA GTG GCT AAT AAA GGG AAA AGC 494  
 Glu Pro Lys Arg Lys Ser Thr Pro Lys Val Ala Asn Lys Gly Lys Ser  
 125 130 135

AAA CAC TAATCTTTTG GTTTTGATGT ACATGTTTTTC AAAAAGTACA TCCTTTTAA 550  
 Lys His  
 140

TCAGTTTACA ATGTAGTTAT GTGACCATGT GGTGTTTAAA TGGATTCCTT TTGGAATTCA 610

TGTATAAATT TACACATTAC ATTTGTGATA CTGAATCTTT TTTTGTCTGA GAAAGATTAA 670

GTTGTCTTTG TTGATTTTCA TATAAAGCAT CATGATGTGT TTAATATTGT AAGATATTCT 730

ATAAGCAGTT GTGAAATCCA AATGTTCTCT GTAAACATTT GTAGTGTTTG AAATGAACAA 790

TGATATTATG AAGTGTGCTA TCTGTAGACC TCGAGGTGTA AGGACATTTG TTTTCAGTAA 850

TGATGAGAAA TACAGTGA CTAAATACCCA CTCTGTTTCT GTTCAGTTAG TTCAACATGT 910

TTCGTGATTT TTTTTTTTTT TTGAGTAATT CTGTCTTGAT ATTCAAAGTC AAAATTGAAA 970

CCTTAAGGCT GTACTTTAAT TCTTCATGTT CCATTTAAAA TAAAATGTTT TCATTAAGTC 1030

TGATGGAAAA 1040

(2) INDICATIONS AS TO ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) KIND: amino acid
- (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Gly Glu Glu Met Asn Glu Asp Tyr Pro Val Glu Ile His Glu  
 1 5 10 15

Ser Leu Thr Ala Leu Glu Ser Ser Leu Gly Ala Val Asp Asp Met Leu  
 20 25 30

Lys Thr Met Met Ala Val Ser Arg Asn Glu Leu Leu Gln Lys Leu Asp  
 35 40 45

Pro Leu Glu Gln Ala Lys Val Asp Leu Val Ser Ala Tyr Thr Leu Asn  
 50 55 60

Ser Met Phe Trp Val Tyr Leu Ala Thr Gln Gly Val Asn Pro Lys Glu

65		70		75		80									
His	Pro	Val	Lys	Gln	Glu	Leu	Glu	Arg	Ile	Arg	Val	Tyr	Met	Asn	Arg
				85					90					95	
Val	Lys	Glu	Ile	Thr	Asp	Lys	Lys	Lys	Ala	Ala	Lys	Leu	Asp	Arg	Gly
			100					105					110		
Ala	Ala	Ser	Arg	Phe	Val	Lys	Lys	Ala	Leu	Trp	Glu	Pro	Lys	Arg	Lys
		115					120					125			
Ser	Thr	Pro	Lys	Val	Ala	Asn	Lys	Gly	Lys	Ser	Lys	His			
	130					135					140				

## (2) INDICATIONS AS TO ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) KIND: nucleotide
- (C) STRAND FORM: single strand
- (D) TOPOLOGY: linear

## (ii) KIND OF MOLECULE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

## (iii) HYPHETICAL: no

## (iv) ANTISENSE: no

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGGGTACCAT GGCAGGTGAA GAAATTAATG AAGACTAT

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## (2) INDICATIONS AS TO ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) KIND: nucleotide
- (C) STRAND FORM: single strand
- (D) TOPOLOGY: linear

## (ii) KIND OF MOLECULE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

## (iii) HYPHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGGTCGACTT AACTTTTACT TTTTCCTTTA TTGGCAAC

38

(2) INDICATIONS AS TO ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) KIND: nucleotide

(C) STRAND FORM: single strand

(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(iii) HYPHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGGGTACCAT GGCAGGTGAA GAAATGAATG AAGATTAT

38

(2) INDICATIONS AS TO ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) KIND: nucleotide

(C) STRAND FORM: single strand

(D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(iii) HYPHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGGTCGACGT GTTTGCTTTT CCCTTTATTA GCCACTTT

38